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Result
No.
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Maximum Match 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
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                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
DB
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877.5
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1: sp_archea:*
2: sp_bacteria
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7:
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  82.3
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Gapop 10.0 ,
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sp_phage:*
sp_plant:*
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sp_vfrus:*
sp_vertebrate:*
sp_unclassified:*
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sp_bacteriap:*
sp_archeap:*
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sp_bacteria:*
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sp_mammal:*
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(without alignments)
575.468 Million cell updates/sec
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        Q9myz9 sus scrofa
Q35545 rattus norv
Q27950 bos indicus
Q28206 bos taurus
Q98206 bos taurus
Q95n13 ovis aries
Q95n14 ovis aries
Q925f5 mus musculu
Q75462 homo sapien
Q9jm58 mus musculu
Q1880 bos taurus
Q46561 ovis aries
Q46600 bos taurus
Q90wg7 cynops pyrr
Q96tf0 homo sapien
Q90wg7
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Q95jf2 a
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90	91	93	94.5	94.5	95.5	95.5	96	96	96	96	96	96	96.5	96.5	96.5	98	98	99	99	99	99	99	99.5	101.5	102.5	102.5	102.5	104.5
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229	608	227	632	615	636	611	1165	958	958	906	896	896	1093	638	390	538	538	1194	1163	925	894	622	1165	848	628	628	628	608
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Q14213	Q99JZ1	Q9GLW3	Q95ML5	Q9DE35	Q90ZI6	Q9PTH9	092921	Q13592	Q92920	Q13593	Q13594	Q92919	070535	Q9TU69	Q9UEH7	09нв91	Q9HBE5	Q9MYL0	Q9MYL2	Q9MYK9	Q9MYL1	Q9N0J7	002671	Q9MZS2	Q9JI97	Q9JKG1	09ЛКТ1	Q9N0Y7
Q14213 homo sapien	Q99jz1 mus musculu	Q9glw3 ursus marit	u,	5		9 xenc	homo	homo	homo		homo	Q92919 homo sapien	070535 rattus norv	cani	homo	Q9hb91 homo sapien	Q9hbe5 homo sapien	macac	macaca		Q9myl1 macaca mula	Q9n0j7 callithrix	002671 sus scrofa	sus scr	cavia		-	Q9n0y7 monodelphis

ALIGNMENTS

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Q9MYZ9 PRELIMINARY;
Q9MYZ9;
O1-OCT-2000 (TrEMBLrel. 15, C:
O1-OCT-2000 (TrEMBLrel. 15, La
O1-DEC-2001 (TrEMBLrel. 19, La
ERYTHROPOIETIN RECEPTOR.
Pfam; PF00041; fn3; 1.

SMART; SM00060; FN3; 1.

PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.

PROSITE; PS00559; MOLYBDOPTERIN_EUK; UNKNOWN_1.

Receptor.

SEQUENCE 509 AA; 55183 MW; 35B565D07C6BCD8A
                                                                                                                                           "Porcine Erythropoietin Receptor: Molecular Cloning and Expression Embryonic and Fetal Liver.";

Domest. Anim. Endocrinol. 0:0-0(2000).

EMBL; AF274305; AAF77065.1; -.

HSSP; P19235; 1EBA.
                                                                                                                                                                                                                 Pearson P.L., Smith T.P.L., S
Christenson R.K., Vallet J.L.
                                                                                                                                                                                                                                                                                                    Sus scrofa (Pig).
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                 InterPro; IPR002996; CR1A.
InterPro; IPR000572; Euk_oxidored_molyb.
InterPro; IPR003528; Hematopo_receptor_L_F1.
                                                                                                                                                                                                                                             TISSUE=LIVER;
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                                                                                                                                                                                                                                                                                      NCBI_TaxID=9823;
 AA; 55183 MW; 35B565D07C6BCD8A CRC64;
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Last annotation update)
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Qy

1 KFESKAALLAARGPEELLCFTERLEDLVCFFEEAASAGVGPGNFSFSFQLEDEPWKLCRL 60

Query Match Best Local Similarity Matches 170; Conserv

Conservative

18;

Score 903.5; DB 6; Pred. No. 3.7e-79; 8; Mismatches 23;

Indels Length 509;

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Best Loc
Matches
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O35545;
O1-JAN-1998 (TremBLrel. 05, Created)
O1-JAN-1998 (TremBLrel. 05, Last sequence update)
O1-DEC-2001 (TremBLrel. 19, Last annotation update)
INTRON 5-INSERTED FORM OF ERYTHROPOIETIN RECEPTOR PI
                                                                                                                                                                                         CHAIN
SEQUENCE
                                                                                                                                                                                                       Signal;
                                                                                                                                                                                                                                                                               Yamaji R., Murakami C., Takenoshita M., Tsuyama S. Miyatake K., Nakano Y.;
"The intron 5-inserted form of rat erythropoietin expressed as a membrane-bound form.";
Biochim. Biophys. Acta 1403:169-178(1998).
                                                                                                                                                                                                                                                                                                        MEDLINE-98296111; PubMed-9630610; MEDLINE-98296111; PubMed-9630610;
                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                      PROSITE;
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InterPro; IPR003961; FN_III.
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                                                                                                                                1 KFESKAALLAARGPEELLCFTERLEDLVCFFEEAASAGVGPGNFSFSFQLEDEPWKLCRL
                                       TRITIAVRARMAEPSFGGFWSAWSEPVSLLT
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                                                                                                                                                                                                                    Pro; IPR003528; Hematopo_receptor_L_F1
Pr00041; fn3; 1.
; SM00060; FN3; 1.
TE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN
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D83509; BAA22373.1; -.
P19235; IEBA.
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165; Conser
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316 1
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316
34220
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Pred. No. 6.8e
23; Mismatches
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                                                                                                                                                                                                                      UNKNOWN_1
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5.8e-77;
hes 22;
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01-DEC-2001
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SEQUENCE
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TISSUE-BONE MARROW;
Suliman H.B., Feldman B.F.,
Submitted (JUN-1996) to the
EMBL; U61399; AAB03871.1;
HSSP; P19235; 1EBA.
                                                                                                Eukaryota; Metazoa; (
Mammalia; Eutheria; (
Bovidae; Bovinae; Bos
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos indicus (Zebu).
Eukaryota; Metazoa; (
Mammalia; Eutheria; (
Bovidae; Bovinae; Bo
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01-DEC-2001 (TrEMBLrel.
ERYTHROPOIETIN RECEPTOR
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                                                                       SEQUENCE FROM N.A.
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PF00041; fn3; 1.
; SM00060; FN3; 1
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P19235; 1EBA.
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FN_III.
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Pred. No. 8.1e-68;
5; Mismatches 25;
                                                                                                                                                                                                                                                              PRT;
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                                            L.L.;
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01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
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InterPro; IPR003961; FN
InterPro; IPR003528; He
Pfam; PF00041; fn3; 1.
SMART; SM00060; FN3; 1.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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Pred. No. 1.7e-61;
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Pred. No. 2e-67;
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C-MPL-II.

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Mus musculus (Mouse).

Theria; Rodentia;
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Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Crani;
Mammalla; Eutheria; Cetartiodactyla
Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
                                                                                                                                                    "Identification and characterization of an isoform of murine Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF36012; AAK52492.1; -
SEQUENCE 566 AA; 63339 MW; A19D3DD5F7BDBA6B CRC64;
                                                                                                                                                                                                                                                                         Sabath D.F., Lofton-Day C., Broudy V.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the ovine fetus.";
Submitted (APR-2001) to the
EMBL; AY029231; AAK38170.1;
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76.4%;
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19,
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; Pred. No. 1.96
14; Mismatches
      28;
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Score 152; DB
Pred. No. 2.2e
28; Mismatches
                                                                                                                                                                                                                                                                                                         Lin
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                              Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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   11;
2-06;
96;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Muridae;
                                                                                                                                                                                                                                                                                                         Kaushansky
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                                                            Length
      Indels
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      42;
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   Gaps
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SKAALLAARGPEELLCFTERLEDLVCFFEEAASAGVGPGNFSFSFQLEDEPWKLCRLHQA 63

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RESULT
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                                                                                                                                             Query Match
Best Local S
Matches 52
                                                                                                                                                                                                              Signal;
SIGNAL
                                                                                                                                                                                                                                                                           Magrangeas F., Jacques Y., Minvielle S.;
"Cloning and expression of a novel soluble protein
hematopoietic cytokine receptor domains.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ datab
EMBL; AF059293; AAC28335.1; -.
EEMBL; AF073515; AAD39681.1; -.
                                                                                                                                                                                                                               InterPro; IPR002996; CR
InterPro; IPR003961; FN
Pfam; PF00041; fn3; 2.
SMART; SM00060; FN3; 2.
                                                                                                                                                                                                                                                                                                                                                            Elson G.C.A., Graber P., Losberger P., Herren S. Menoud L.N., Wells T.N.C., Kosco-Vilbois M.H., G "CLF-1, a Novel Soluble Protein Shares Homology Cytokine Type-I Receptor Family.";
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOKINE-LIKE CLF-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CYTOKINE-LIKE FACTOR-1 PRECURSOR.
                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       075462;
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                                                                                                                                                                                                                                                                      HSSP;
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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             172
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   CVLSNLRGRTRITIAVRARMAEPSFG-----
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                              VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSV-----DWKVVDDVSNQTS
                                                  L-VARLADESGHVVIRWLPPPET----
                                                                                                                          PEELLCFTERLEDLVCFFEEAASAGVGPG-----NFSFSFQLEDEPW----KLCRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RTECVLSNLRGRTRITIAVRARMAEPSFGGFWSAWSEPVSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTARGAIRFWCSLPTAD-TSSFVPLELRLTAAS-GAPRFHRVIHI------
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                                                                                                        PVNISCWSKNMKDLTCRWT-----PGAHGETFLHTNYSLKYKLR----WYGQDNTCEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---CLVSGLQAGKSYWLQLRSQPDGVSLRGSWGPWSFPVTV 211
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                                                                                                                                                                                                                                                                     P16471; 1BP3
                                                                                                                                             ch 11.2%;
l Similarity 22.9%;
52; Conservative 3
                                                                                                                                                                                                                      Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                     /s (Human).
Metazoa; Chordata; C
- Lheria; Primates; (
                                                                                                                                                                                            38
422 AA;
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                                                                    -CHIP-KDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD
                                                                                                                                                                                                               37
                                                                                                                                                                                                                                                CR1A.
FN_III.
                                                                                                                                                                                            46301 MW;
                                                                                                                                              36;
                                                                                                                                            Score 122.5; DB 4;
Pred. No. 0.0011;
6; Mismatches 84;
                                                                                                                                                                                           POTENTIAL.
CYTOKINE-LIKE FACTOR-1
AD9DEFCB01B84228 CRC6
                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                PMTSHIRFELDISAGNGAGSVQRVELLEGRTE
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            -GFWSAWSEPVSLLT
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                                                                                                                                                              DB 4;
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., Gauchat J.F.;
ogy With Members
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                                                                                                                                                                                            CRC64;
                                                                                                                                                              Length
                                                                                                                                              Indels
             211
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                                                                                                                                                                                  RESULT
Q9JM58
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Q9UHH5
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Query Match
Best Local S
Matches 52
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InterPro; IPR002996; C
InterPro; IPR003961; E
InterPro; IPR003961; E
Pfam; PF00041; fn3; 2;
SMART; SM00060; FN3; ;
            SEQUENCE FROM N.A. Hiroyama T., Iwama A., Nakamura Y., "cytokine receptor like molecule 3. Submitted (MAR-2000) to the EMBL/Genembl; AB040038; BAA92777.1; -. HSSP; P16471; 1BP3.
                                                                                                                                                                                    CYTOKINE RECEPTOR CRLF1 OR CRLM3.
                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                        Mammalia; Eutheria;
                                                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                   Q9JM58;
                                                                                                                                                                                                                                                                                 Q9JM58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lok S., Presnell S.R., Jelmberg A.C., Gilbert T Foster D.C., Adams R.L., Lehner J.M., O'Hara P. Submitted (AUG-1999) to the EMBL/GenBank/DDBJ d EMBL, AF178684; AAD54385.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASS I CYTOKINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9UHH5
                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                10
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MGI:1340030;
                                                                                                                                                                                                                                                                                                                                                             CRLAGLKPGTVYFVQVRCN---
                                                                                                                                                                                                                                                                                                                                                                                          CVLSNLRGRTRITIAVRARMAEPSFG-----GFWSAWSEPVSLLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       L-VARLADESGHVVIRWLPPPET----PMTSHIRFELDISAGNGAGSVQRVELLEGRTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YHTVGPHS-----CHIP-KDLALETPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HQAPTARGAIRFWCSLPTADTSSFVPLELRLTAAS--GAPRFH-RVIHINEVVLLDAPVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity 22.9
52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Metazoa;
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                                                                                                                                                                                                                                                                                 PRELIMINARY;
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Crlf1
                                                                                                                                                                                                    LIKE
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2
                                                                                                                                    Chordata;
Rodentia;
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Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46315
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FN_III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.1%; 22.9%;
                                                                                                                                                                                                    . 15, Created)
. 15, Last sequence update)
. 19, Last annotation updat
. MOLECULE 3 PRECURSOR.
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13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW;
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Last sequence up
Last annotation
                                                                                                                                                                                                                                                                                                                                                             -PFGIYGSKKAGIWSEWSHPTAAST
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                                              EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 121.5; DB Pred. No. 0.0014; 6; Mismatches 8
                                                                                                                                       Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; V
Catarrhini;
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PROLACTIN RECEPTOR SHORT FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Endocrinology 138:3187-3194(1997).
EMBL; AF027403; AAB83999.1; -.
HSSP; P14787; 1AN3.
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MEDLINE=97375450; PubMed=9231767;
Schuler L.A., Nagel R.J., Gao J.,
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Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00041; fn3; 2. SMART; SM00060; FN3; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissues."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 L-VARLADESGHVVIRWLPPPET-----PMTSHIRFELDISAGNGAGSVQRVELLEGRTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 YHTVGPHS-----CHIP-KDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPD
                                            63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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CPDYKTGGPNSCYFSKKHTSIWKMYVITVNAINQMGISSSDPLY---VHVTYIVEPEPPA 131
                                         APTARGAIRFWCSLPTADTSSFVPLELRLTA-----ASGAPRFHRVIHINEVVLLDAPV
                                                                                     SLLNGQSPPEKPKLVKCRSPGKETFTCWWEPGADGGL-PTNYTLTYHKEGE----TLIHE
                                                                                                                                  ALLAARGPEE-----LLCFTERLEDLVCFFEEAASAGVGPGNFSFSFQLEDEPWKLCRLHQ
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IPR003528;
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FN_III.
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                                                                                                                                                                                   Score 118; DB
Pred. No. 0.00
40; Mismatches
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Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL. 910535C629CA7056 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                    9F1C15FB41DE0787 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bovine fetal and maternal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                296
                                                                                                                                                                 J.002;
101;
                                                                                                                                                                                                                               DB 6;
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                                                                                                                                                                                                                            Length 296;
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                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                         CC --- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN (BY SIMILARITY).
CC --- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC --- ALTERNATIVE PRODUCTS: THREE ISOFORMS; LONG ISOFORM (L-OPR) (SHOWN
CC HERE), SHORT ISOFORM (S-OPR) AND SOLUBLE ISOFORM; ARE PRODUCED BY
CC ALTERNATIVE SPLICING.
CC --- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED (LIVER,
CC --- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED (LIVER,
CC --- SIMILARITY: ONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC --- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC --- SIMILARITY: AAB96795.1; --
CR EMBL; AF041257; AAB96795.1; --
CR EMBL; AF041257; AAB96795.1; --
CR EMBL; AF041258; AAB97744.1; --
CR EMBL; AF041258; AAB97744.1; --
CR EMBL; AF042358; AAB97744.1; --
CR EMBL; AF042358; AAB97745.1; --
CR EMBL; AF041297; AAB96755.1; --
CR EMBL; AF041297; CAA7156.1; --
CR EMBL; AF041277; AAB9675.1; --
CR EMBL; AF041278; CAA7156.1; --
CR EMBL; AF041277; AAB96782.1; --
CR EMBL; AF041278; CAA7156.1; --
CR EMBL; AF041277; AAB96782.1; --
CR EMBL; AF041278; CAA7156.1; --
CR EMBL; AF041277; AAB96782.1; --
CR EMBL; AF041278; CAA71766.1; --
CR EMBL; AF041277; AAB96782.1; --
CR EMBL; AF041277; AAB96782.1; --
CR EMBL; AF041278; CAA71766.1; --
CR EMBL; AF041277; AAB96782.1; --
CR EMBL; AF041277; AAB96782.1; --
CR EMBL; AF041277; AAB96782.1; --
CR EMBL; AF041278; CAA71766.1; --
CR EMBL; AF041277; AAB96782.1; --
CR EMBL; AF041277; AAB96782.1; --
CR EMBL; AF041277; AAB96782.1; --
CR EMBL; AF041278; CAA71766.1; --
CR EMBL; AF041278; AAR97744.1; --
CR EMBL; AF041278; AAR97749.1; --
C
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TISSUE-MAMMARY GLAND, AND LIVER;
MEDLINE-98001468; PubMed-934303;
Bignon C., Binart N., Ormandy C., Schuler L.A., Kelly P.A., Djiane
"Long and short forms of the ovine prolactin receptor: cDNA clonir
and genomic analysis reveal that the two forms arise by different
alternative splicing mechanisms in ruminants and in rodents.";
J. Mol. Endocrinol. 19:109-120(1997).
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Caprinae; Ovis.

NCBI_TaxID=9940;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anthony R.V., Smith G.W., Duong A., Pratt S.L., Smith M.F.; "Two forms of the prolactin receptor messenger ribonucleic acid are present in ovine fetal liver and adult ovary."; Endocrine 3:291-295(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pituitary gland and visualization of the specific translation signal in gonadotrophs."; endocrinology 139:5215-5223(1998).
                                      Pfam; PF00041; fn3; SMART; SM00060; FN3
                                                                                                              InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III
InterPro; IPR003528; Hemator
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 61-395 FROM N.A., AND ALTERNATIVE SPLICING. STRAIN-SCOTTISH BLACKFACE / ISOLATE M22/80; TISSUE-ANTERIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190
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    PS01352;
                                          FN3;
HEMATOPO_REC_L_F1; UNKNOWN_1
                                  2.
                                                                                                                       Hematopo_receptor_L_F1
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01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SOMATOTROPIN RECEPTOR 1B PRECURSOR.
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bowandlia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovinae; Bovinae; Bos.
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                     InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN III.
InterPro; IPR0039528; Hematopo
Pfam; PF00041; fn3; 1.
SMART; SM00060; FN3; 1.
                                                                                                                            "Bovine somatotropin receptor 1B mRNA.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ
EMBL; AF044258; AAC025544.1; -.
HSSP; P10912; 1A22.
                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-HOLSTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Receptor; T:
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PROSITE;
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49; Conserv
  M00060; FN3;
PS01352; HE
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      HEMATOPO_REC_L_F1; UNKNOWN_1
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CYTOPLASMIC (POTENTIAL FIBRONECTIN TYPE-III. FIBRONECTIN TYPE-III.
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BY SIMILARITY.
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
QOSPPEKPKLIKCRSPCKETFTCWWEPCADGGLPTNTLTY
RK -> ASLYVPGGKCSSVCTYMAYPFVGGIFLHMYLCVDQ
YLLLTVTS (IN SOLUBLE ISOFORM).
MISSING (IN SOLUBLE ISOFORM).
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1 -> V (IN AAB97744).
E -> K (IN REF. 2).
E C534FDE538837A0 CRC64;
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Q96TFO;
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01-DEC-2001 (TrEMBLrel. 19, C
01-DEC-2001 (TrEMBLrel. 19, L
01-DEC-2001 (TrEMBLrel. 19, L
PROLACTIN RECEPTOR PRECURSOR.
                                                                                                                                                                                                                                                                                                              Yamamoto T., Nakayama Y., Matsuda Y., Abe S.-I.; "Cloning and expression of a cDNA encoding a prolactin Japanese red-beliled newt, Cynops pyrrhogaster."; Zool. Sci. 15:741-747(1998).
                                                                                                                                                                                                                                                                                                                                                                                                          Cynops pyrrhogaster (Japanese common newt).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
                                                                                                                                                                                                                                                                                                     Signal;
                                                                                                                                                                                                                                                                                                                                                                                                Amphibia; Batrachia;
NCBI_TaxID=8330;
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                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                    TISSUE=KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                 NSCYFNSSYTSVWTPYCIKLTSNGGIVD-HKCFSVEDIVQPDPPVGLNWTLLNISLTEIH
                                                                        RGRTRITIAVRARMAEPSFGGFWSAWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FWCSLPTADTSSFVPLELRLTAASGAPRFHRVIHINEVVLLDAPVGLVARLADES-----
                                                                                                    HLLVKWSPPSEADVKSGWVTIEYEVQFKSKKAKEWETLTAGKQRQLKVF
                                                                                                                        HVVIRWLPPPETPMTS---HIRFELDISAGNG-----AGSVQRVELLEGRTECVLSNL
                                                                                                                                              CFFDKKHTSIWTMYNIIVNATNELGSTTSDPKF
                                                                                                                                                                CSLPTADTSSFVPLEL-----RLTAASGAPRFHRVIHINEVVLLDAPVGLVARLADESG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PKFTKCRSPELETFSCHWTDGANHSLQSPGSVQMFYIRRDIQEWKEC----
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l Similarity 26.3%;
35; Conservative 2
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40; Conserv
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634 AA;
                                                                                                                                                                                                                                                                                 626 AA;
                                                                                                                                                                                                                                Conservative
          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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634 S
70914 MW;
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                                                                                                                                                                                                                                                                                 26
69944 MW;
                                                                                                                                                                                                                                       10.2%;
                                                                                                                                                                                                                                42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence up
                                                                                                                                                                                                                             Score 111.5; DE Pred. No. 0.021; 2; Mismatches
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                                                                                                                                                                                                                                                                                 POTENTIAL.

B6050DD9C9F58DE5 CRC64;
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SOMATOTROPIN RECEPTOR 1B.
; 176936D32EA7C4C9 CRC64;
          PRT;
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          521
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Best Local Similarity
Matches 53; Conserv
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MEDLINE-2012249; PubMed=10655549;
MEDLINE-20122249; PubMed=10655549;
Ciccodicola A., D'Esposito M., Esposito T., Gianfrancesco F.,
Migliaccio C., Miano M.G., Matarazzo M.R., Vacca M., Franze A.,
Cuccurese M., Cocchia M., Curci A., Terracciano A., Torino A.,
Cuccurese M., Mercadante G., Pannone E., Archidiacono N., Rocchi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUÊNCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schlessinger D., D'Urso M.;
"Differentially regulated and evolved genes in the fully sequenced Xq/Yq pseudoautosomal region.";
Hum. Mol. Genet. 9:395-401(2000).
EMBL; AJ271736; CAB96817.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TremBLrel.
01-DEC-2001 (TremBLrel.
01-DEC-2001 (TremBLrel.
01-DEC-2001 (TremBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                      209
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                                                                                                                                                                                                                                                 70 IRFWCSLPTADTSSFVPLELRLTAASG-APRFHRVIHINEV------VLLDAP 115
                                                                                                                                                                                                                                                                                         47
                                                                                                                                                                                                                                                                                                                  12 RGPEE--LLCFTERLEDLVCFFEEAASAGVGPGNFSFSFQLEDEPWKLCRLHQAPTARGA 69
                                                                                                                                                ----CILRGSECTVVLPPEAVLVPSDNFTTTFHHCMSGREQVSLVDPEYLPRRHVKLDPP 150
                                                                                  LEAFELDPGFIHEARLRVQMATLEDDVVEEERYTGQWSEWSQPV
                                                                                                                LSNL-----RGRTRITIAVRAR--MAEPSFGGFWSAWSEPV 207
                                                                                                                                                                                                                                                                                      QGPRSRTFTCLTNNILRIDCHW-SAPELGQG-----SSPWLLFTSNQAPGGTHK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                             521 AA;
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                       10.1%; Score 111; DB 4; Length 521; 23.7%; Pred. No. 0.019; ative 28; Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           57146 MW; 07C40436466173F3 CRC64;
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. 19, Last sequence. 19, Last annotation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                     46; Gaps
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